

results of BLAST

BLASTX 2.2.8 [Jan-05-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1082491251-5369-38913976047.BLASTQ3

Query=

(1578 letters)

Database: All non-redundant GenBank CDS

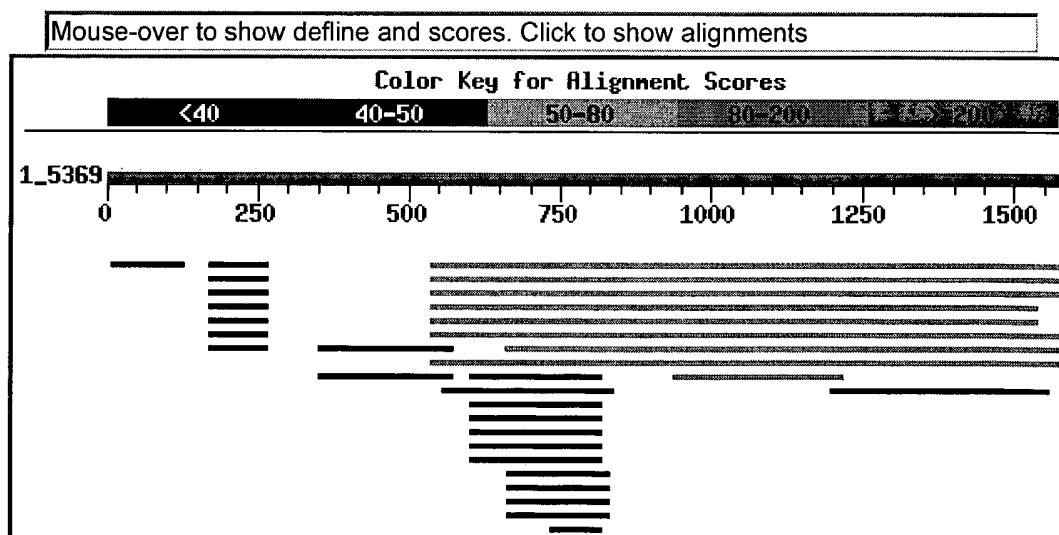
translations+PDB+SwissProt+PIR+PRF

2,768,312 sequences; 778,115,222 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 64 Blast Hits on the Query Sequence



Sequences producing significant alignments:

Score E
(bits) Value

gi 17999520 ref NP_542119.1 	vesicular inhibitory amino aci...	76	5e-25	L
gi 29428243 sp Q95KE2 VIAA_MACFA	Vesicular inhibitory amino...	75	1e-24	
gi 29428127 sp O35633 VIAA_MOUSE	Vesicular inhibitory amino...	73	4e-23	L

gi 26665359 dbj BAC44888.1 	vesicular GABA transporter a fo...	<u>73</u>	4e-23	
gi 13929106 ref NP_113970.1 	vesicular inhibitory amino aci...	<u>72</u>	6e-23	L
gi 6678569 ref NP_033534.1 	vesicular inhibitory amino acid...	<u>73</u>	4e-22	L
gi 34785016 gb AAH36458.2 	VIAAT protein [Homo sapiens]	<u>69</u>	2e-21	L
gi 34785895 gb AAH57733.1 	MGC68938 protein [Xenopus laevis]	<u>59</u>	2e-17	L
gi 19744862 gb AAL96689.1 	solute carrier family 32 member ...	<u>57</u>	1e-06	
gi 31793484 ref NP_855977.1 	POSSIBLE CONSERVED MEMBRANE PR...	<u>37</u>	1.0	
gi 41353676 emb CAE55465.1 	POSSIBLE CONSERVED MEMBRANE PRO...	<u>37</u>	1.0	
gi 17368397 sp P97260 SCAP_CRIGR	Sterol regulatory element ...	<u>37</u>	1.8	
gi 40254240 ref NP_766336.2 	hypothetical protein 603043001...	<u>37</u>	1.8	L
gi 26327313 dbj BAC27400.1 	unnamed protein product [Mus mu...	<u>37</u>	1.8	L
gi 31418626 gb AAH53109.1 	603043001 protein [Mus musculus]	<u>37</u>	1.8	L
gi 42734337 ref NP_061958.1 	hypothetical protein DKFZp434K...	<u>36</u>	2.3	L
gi 21758894 dbj BAC05410.1 	unnamed protein product [Homo s...	<u>36</u>	2.3	L
gi 34859315 ref XP_219356.2 	similar to hypothetical protei...	<u>36</u>	3.0	L
gi 44624381 gb EAK56287.1 	unknown [environmental sequence]	<u>36</u>	3.0	
gi 115206 sp P11586 C1TC_HUMAN	C-1-tetrahydrofolate synthas...	<u>36</u>	3.0	L
gi 13699868 ref NP_005947.2 	methylenetetrahydrofolate dehy...	<u>36</u>	3.0	L
gi 30048109 gb AAH50420.1 	Methylenetetrahydrofolate dehydr...	<u>36</u>	3.0	L
gi 37805836 dbj BAC99471.1 	hypothetical protein [Oryzasat...	<u>35</u>	4.0	
gi 19850913 gb AAL99692.1 	C1-tetrahydrofolate synthase [Mu...	<u>34</u>	8.8	L
gi 111430 pir A35367	methylenetetrahydrofolate dehydrogena...	<u>34</u>	8.8	
gi 26335437 dbj BAC31419.1 	unnamed protein product [Mus mu...	<u>34</u>	8.8	L
gi 11968082 ref NP_071953.1 	C1-tetrahydrofolate synthase [...]	<u>34</u>	8.8	L
gi 26348793 dbj BAC38036.1 	unnamed protein product [Mus mu...	<u>34</u>	8.8	L
gi 34871548 ref XP_222019.2 	similar to RIKEN cDNA 9430031J...	<u>34</u>	8.8	L
gi 37537544 ref NP_780730.2 	RIKEN cDNA 6430598A04 gene [Mu...	<u>34</u>	8.8	L
gi 26328379 dbj BAC27928.1 	unnamed protein product [Mus mu...	<u>34</u>	8.8	L
gi 40363747 dbj BAD06308.1 	vesicular GABA transporter [Cio...	<u>30</u>	9.6	

Alignments

☐ >[gi|17999520|ref|NP_542119.1|](#) **L** vesicular inhibitory amino acid transporter; GAB transporter; vesicular GABA transporter [Homo sapiens]
[gi|29428257|sp|Q9H598|VIAA_HUMAN](#) Vesicular inhibitory amino acid transporter (GAB transporter) (Vesicular GABA transporter) (hVIAAT)
[gi|13396317|emb|CAC15529.2|](#) **L** ba12201.1 (A novel protein (ortholog of the mouse v inhibitory amino acid transporter, VIAAT)) [Homo sapiens]
[gi|16549700|dbj|BAB70846.1|](#) **L** unnamed protein product [Homo sapiens]
[gi|17975777|gb|AAK98782.1|](#) **L** vesicular inhibitory amino acid transporter [Homo sa
[gi|31566392|gb|AAH53582.1|](#) **L** Vesicular inhibitory amino acid transporter [Homo sa
 Length = 525

Score = 76.3 bits (186), Expect(2) = 5e-25

Identities = 95/314 (30%), Positives = 106/314 (33%), Gaps = 101/314 (32%)

Frame = +1

Query: 580 FARMGFQAATDEEXXXXXXXXXXXXXXXXXDE-----SPAGTRALKRP-----SR 699
 FARMGFQAATDEE + P G + P R
 Sbjct: 28 FARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKAEGEPCGDEGAEAPVEGDIHYQR 87

Query: 700 GSGAPLPPSGSKD-IRGPRQAQNH-----GVGAPSRACSCWAYPTP----- 819
 GSGAPLPPSGSKD + G + H G + + P
 Sbjct: 88 GSGAPLPPSGSKDQVGGGGEFEGGHDKPKITAWAGWNVNNAIQGMFVLGLPYAILHGGYL 147

Query: 820 GLFLIIFAAAXXXXXXXXXXXXXXXXXXXXXXXXXXSQ-----R 939
 GLFLIIFAA S
 Sbjct: 148 GLFLIIFAAVCCYTGKILIACLYEENEDGEVVRVRSYVAIANACCAPRFPTLGGRVNVN 207

Query: 940 VAQIIELVMTCILPHV-----QQLPGA-----ARVAARPCCLA---PSLRTS 1059
 VAQIIELVMTCIL V PG A PC L + S
 Sbjct: 208 VAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQKWSIIATAVLLPCAFLKNLKAVSKFS 267

Query: 1060 LLCTLAHFVINIL-----SSPRLGLGEGQVLPSPASSCSATRL 1176
 LLCTLAHFVINIL + + G ++ S S L
 Sbjct: 268 LLCTLAHFVINILVIAYCLSRARDWAWEKVKFYIDVKKFPISIGIIVFS-YTSQIFLPSL 326

Query: 1177 RGNMQPSEFHCMM 1218
 GNMQPSEFHCMM
 Sbjct: 327 EGNMQPSEFHCMM 340

Score = 76.3 bits (186), Expect = 2e-12

Identities = 88/262 (33%), Positives = 99/262 (37%), Gaps = 85/262 (32%)

Frame = +3

Query: 537 SKLSNVATSVSNKS-VRQDG-FXXXXXXXXXXXXXXXXXC-----R 656
 SKLSNVATSVSNKS + G F C
 Sbjct: 7 SKLSNVATSVSNKSQAKMSGMFARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKAE 66

Query: 657 *EPCGDEGAEAPVE----RQRSSAALRLQGH-----GATTSPKSRR-----G 776
 EPCGDEGAEAPVE QR S A L G G PK
 Sbjct: 67 GEPCGDEGAEAPVEGDIHYQRGSGAPLPPSGSKDQVGGGGEFEGGHDKPKITAWAGWNVN 126

Query: 777 SAIQGMFVLGLPYAGVVSHLRRRCVLPRAC----TRRMKTA-----RW 896
 +AIQGMFVLGLPYA + +L ++ A T ++ A +
 Sbjct: 127 NAIQGMFVLGLPYAILHGGYLGLFLIIFAAVCCYTGKILIACLYEENEDGEVVRVRSY 186

Query: 897 WAIANACCAPRFPTRSADHRAGDDVHPASCTTASRG----- 1007
 AIANACCAPRFPT G V+ A C
 Sbjct: 187 VAIANACCAPRFPT-----LGGRVVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQK 241

Query: 1008 --PCRSTAVLLPCAFLKNLSAV 1067
 +TAVLLPCAFLKNL AV
 Sbjct: 242 SWSIIATAVLLPCAFLKNLKAV 263

Score = 69.7 bits (169), Expect = 2e-10

Identities = 118/441 (26%), Positives = 134/441 (30%), Gaps = 152/441 (34%)

Frame = +2

Query: 620 DDLD FEHRQGLQMXXXXXX-----XXXXXXXXXXXXXXXXXCRPPAPRT----- 739
 DDLD FEHRQGLQ M P P +
 Sbjct: 48 DDLD FEHRQGLQMDILKAEGEPCGDEGAEAPVEGDIHYQRGSGAPLPPSGSKDQVGGGGE 107

Query: 740 FGGHDKPKITAWERH-----PGHVRAGPTLRRGCFXXXXXXX----- 853
 FGGHDKPKITAW E P + G L G F
 Sbjct: 108 FGGHDKPKITAW EAGWNV TNAIQGMFVLGLPYAILHGGYL--GLFLIIFAAVVCCYTGKI 165

Query: 854 XXXXXYEENEDGEVV-----GHSQRLLRPALPN----A*XXXXXXXXXASC----- 979
 YEENEDGEVV + P P +C
 Sbjct: 166 LIACLYEENEDGEVVRV RDSYVAIANACCAPRFPTLGGRVVNVAQIIELVMTCILYVVVS 225

Query: 980 --LMYNSFPGLPVSQHG---RAAALRLP*EPLCCALWPTSSSIS----- 1096
 LMYNSFPGLPVSQ A A+ LP CA ++S
 Sbjct: 226 GNLMYNSFPGLPVSQKSWSI IATAVLLP-----CAFLKNLKA VSKFSL LCTLAHFVINIL 280

Query: 1097 -----CPPRDWAW EKVKFY-----HLHWHHRVQLHVSGXXXX-----XX 1198
 RDWAW EKVKFY + + + Q+ +
 Sbjct: 281 VIAYCLSRARDWAW EKVKFYIDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSEFHCMM 340

Query: 1199 XXXXXXXXVLKGLFALVAYXXXXXX-----XXXXXXXXXXXXXXXXXXXXSLP--- 1339
 VLKGLFALVAY LP
 Sbjct: 341 NWT HIAACVLKGLFALVAYLTWADETKEVITDNLPGSIRAVVNIFLVAKALLSYPLPFFA 400

Query: 1340 -----SLFQEGSRAFFPAPEVLGADAALRARPFMCR T SRC S----- 1447
 SLFQEGSRAFFPA D L++ T RC+
 Sbjct: 401 AVEVLEKSLFQEGSRAFFPA--CYSGDGR LKSWGL---TLRCALVVFTLLMAIYVPHFAL 455

Query: 1448 -----WASPLCFL LPSLF 1486
 + LCFL LPSLF
 Sbjct: 456 LMGLTGS L TGAGLCFL LPSLF 476

Score = 62.8 bits (151), Expect (2) = 5e-25

Identities = 52/136 (38%), Positives = 60/136 (44%), Gaps = 41/136 (30%)

Frame = +3

Query: 1254 TSEVITDNLPGSIRAGQGA VVLSSAILC-----RRSSRKAAAPFS 1373
 T EVITDNLPGSIRA +++ A+L R+ A
 Sbjct: 366 TKEVITDNLPGSIRAVVNIFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAFFPACYS GD 425

Query: 1374 RPLKSWGLTLRCALVHLCAALRAAHGPH-----PSVSCC---PASF-----T 1490
 LKSWGLTLRCALV + L A + PH C P+ F
 Sbjct: 426 GR LKSWGLTLRCALV-VFTLLMAIYVPHFALLMGLTGS L TGAGLCFL LPSLFHLRLLWRK 484

Query: 1491 CAWHQVFFDVAIFVIG 1538
 WHQVFFDVAIFVIG
 Sbjct: 485 LLWHQVFFDVAIFVIG 500

Score = 35.8 bits (81), Expect = 3.0

Identities = 27/74 (36%), Positives = 28/74 (37%), Gaps = 20/74 (27%)

Frame = +1

Query: 1417 SIYVPHFALLMGLTPLFLAA-----QPLXXXXXXXXXXXXXXXXXXXX 1536
 +IYVPHFALLMGLT A
 Sbjct: 447 AIYVPHFALLMGLTGS L TGAGLCFL LPSLFHLRLLWRKLLWHQVFFDVAIFVIGGICSVS 506

Query: 1537 XFVHSLEGLIEAYR 1578
 FVHSLEGLIEAYR
 Sbjct: 507 GFVHSLEGLIEAYR 520

☐ >gi|29428243|sp|Q95KE2|VIAA_MACFA Vesicular inhibitory amino acid transporter (G transporter) (Vesicular GABA transporter)
 gi|14388326|dbj|BAB60726.1| hypothetical protein [Macaca fascicularis]
 Length = 525

Score = 75.5 bits (184), Expect(2) = 1e-24
 Identities = 96/314 (30%), Positives = 106/314 (33%), Gaps = 101/314 (32%)
 Frame = +1

Query: 580 FARMGFQAATDEEXXXXXXXXXXXXXXDE-----SPAGTRALKRP-----SR 699
 FARMGFQAATDEE + P G + P R
 Sbjct: 28 FARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKAEGEPCGDEGAEPPEVEGDIHYQR 87

Query: 700 GSGAPLPPSGSKDIRG-----PR-QAQNHGVGAPSRACSCWAYPTP----- 819
 GSGAPLPPSGSKD G P+ A G + + P
 Sbjct: 88 GSGAPLPPSGSKDQVGAGGEFGGHDKPKITAWAEGWNVNTNAIQGMFVLGLPYAILHGGYL 147

Query: 820 GLFLIIIFAXXXXXXXXXXXXXXXXXXXXXXXXXXSQ-----R 939
 GLFLIIIFAA S
 Sbjct: 148 GLFLIIIFAAVCCYTGKILIACLYEENEDGEVVRVDRSYVAIANACCAPRFPPTLGGRVVN 207

Query: 940 VAQIIELVMTCILPHV-----QQLPGA-----ARVAARPCCLA---PSLRTS 1059
 VAQIIELVMTCIL V PG A PC L + S
 Sbjct: 208 VAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQKSWSIATAVLLPCAFLKLNKAVSKFS 267

Query: 1060 LLCTLAHFVINIL-----SSPRLGLGEGQVLPSPASSCSATRL 1176
 LLCTLAHFVINIL + + G ++ S S L
 Sbjct: 268 LLCTLAHFVINILVIAYCLSRARDWAWEKVKFYIDVKKFPISIGIIVFS-YTSQIFLPSL 326

Query: 1177 RGNMQQPSEFHCMM 1218
 GNMQQPSEFHCMM
 Sbjct: 327 EGNMQQPSEFHCMM 340

Score = 73.6 bits (179), Expect = 1e-11
 Identities = 86/262 (32%), Positives = 97/262 (37%), Gaps = 85/262 (32%)
 Frame = +3

Query: 537 SKLSNVATSVSNKSVRQDG--FXXXXXXXXXXXXXXXXXC-----R 656
 SKLSNVATSVSNKS + F C
 Sbjct: 7 SKLSNVATSVSNKSQAKVSGMFARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKAE 66

Query: 657 *EPCGDEGAEPVE----RQRSSAALRLQHS-----GATTSPKSRR-----G 776
 EPCGDEGAEPVE QR S A L G G PK
 Sbjct: 67 GEPCGDEGAEPPEVEGDIHYQRGSGAPLPPSGSKDQVGAGGEFGGHDKPKITAWAEGWNV 126

Query: 777 SAIQGMFVLGLPYAGVVSHHLRRRCVLPAC----TRRMKTA-----RW 896
 +AIQGMFVLGLPYA + +L ++ A T ++ A +
 Sbjct: 127 NAIQGMFVLGLPYAILHGGYLGLFLIIIFAAVCCYTGKILIACLYEENEDGEVVRVDRSY 186

Query: 897 WAIANACCAPRFPTRADHRAGDDVHPASCTTASRGC----- 1007
 AIANACCAPRFPT G V+ A C
 Sbjct: 187 VAIANACCAPRFPT-----LGGRVVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQK 241

Query: 1008 --PCRSTAVLLPCAFLKNLSAV 1067
 +TAVLLPCAFLKNL AV
 Sbjct: 242 SWSIIATAVLLPCAFLKLNKAV 263

Score = 72.4 bits (176), Expect = 3e-11
 Identities = 120/441 (27%), Positives = 135/441 (30%), Gaps = 152/441 (34%)
 Frame = +2

Query: 620 DDLDFEHRQGLQXXXXXXXXX-----XXXXXXXXXXXXCRPP-----APRT 739
 DDLDFEHRQGLQM PP A
 Sbjct: 48 DDLDFEHRQGLQMDILKAEGEPCGDEGAEPPEVDIHYQRGSGAPLPPSGSKDQVGAGGE 107

Query: 740 FGGHDKPKITAWERH-----PGHVRAGPTLRRCGCFXXXXXXXXX----- 853
 FGGHDKPKITAW E P + G L G F
 Sbjct: 108 FGGHDKPKITAW EAGWNVTNAIQGMFVLGLPYAILHGGYL--GLFLIIFA VVCCYTGKI 165

Query: 854 XXXXXYEENEDGEVV-----GHSQRLLRPALPN---A*XXXXXXXXXASC----- 979
 YEENEDGEVV + P P +C
 Sbjct: 166 LIACLYEENEDGEVVRVRSYVAIANACCAPRFP T L GGRVVNVAQIIELVMTCILYVVVS 225

Query: 980 --LMYNSFPGLPVSQHG---RAAALRLP*EPLCCALWPTSSSIS----- 1096
 LMYNSFPGLPVSQ A A+ LP CA ++S
 Sbjct: 226 GNLMYNSFPGLPVSQKWSIIATAVLLP-----CAFLK NLKAVSKFSL LCTLAHFVINIL 280

Query: 1097 -----CPPRDWAWEKVKFY-----HLHWHHRVQLHVS GXXXXX-----XX 1198
 RDWAWEKVKFY + + + Q+ +
 Sbjct: 281 VIAYCLSRARDWAWEKVKFYIDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSEFHCMM 340

Query: 1199 XXXXXXXXVLKGLFALVAYXXXXXXXX-----XXXXXXXXXXXXXXXXXXXXSLP--- 1339
 VLKGLFALVAY LP
 Sbjct: 341 NWT HIAACVLKGLFALVAYLTWADETKEVITDNLPGSIRAVVNI FLVAKALLSYPLPFFA 400

Query: 1340 -----SLFQEGSRAFFPAPEVLGADAALRARPFMCRTSRCS----- 1447
 SLFQEGSRAFFPA G D L++ T RC+
 Sbjct: 401 AVEVLEKSLFQEGSRAFFPA--CYGGDGR LKSWGL---TLRCALVVFTLLMAIYVPHFAL 455

Query: 1448 -----WASPLCFL LPSLF 1486
 + LCFL LPSLF
 Sbjct: 456 LMGLTGSLTGAGLCFL LPSLF 476

Score = 62.4 bits (150), Expect(2) = 1e-24
 Identities = 52/136 (38%), Positives = 60/136 (44%), Gaps = 41/136 (30%)
 Frame = +3

Query: 1254 TSEVITDNLPGSIRAGQGA VV LSSAILC-----RRSSRKAAAPFS 1373
 T EVITDNLPGSIRA +++ A+L R+ A
 Sbjct: 366 TKEVITDNLPGSIRAVVNI FLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAFFPAC YGGD 425

Query: 1374 RPLKSWGLTLRCALVHLCAALRAAHGPH-----PSVSCC---PASF-----T 1490
 LKSWGLTLRCALV + L A + PH C P+ F
 Sbjct: 426 GR LKSWGLTLRCALV-VFTLLMAIYVPHFALLMGLTGSLTGAGLCFL LPSLFHLRL LWRK 484

Query: 1491 CAWHQVFFDVAIFVIG 1538
 WHQVFFDVAIFVIG
 Sbjct: 485 LLWHQVFFDVAIFVIG 500

Score = 35.8 bits (81), Expect = 3.0

Identities = 27/74 (36%), Positives = 28/74 (37%), Gaps = 20/74 (27%)
Frame = +1

Query: 1417 SIYVPHFALLMGLTPLFLAA-----QPLXXXXXXXXXXXXXXXXXXXX 1536

+IYVPHFALLMGLT A

Sbjct: 447 AIYVPHFALLMGLTGSLTGAGLCFLPSLFHLRLLWRKLLWHQVFFDVAIFVIGGICSVS 506

Query: 1537 XfvhsLEGLIEAYR 1578

FVHSLEGLIEAYR

Sbjct: 507 GFVHSLEGLIEAYR 520

☐ >gi|29428127|sp|O35633|VIAA_MOUSE ☒ Vesicular inhibitory amino acid transporter
transporter) (Vesicular GABA transporter) (mVIAAT)
(mVGAT)

gi|26665360|dbj|BAC44889.1| ☒ vesicular GABA transporter b form [Mus musculus]

gi|30354125|gb|AAH52020.1| ☒ Viaat protein [Mus musculus]

Length = 525

Score = 72.8 bits (177), Expect = 2e-11

Identities = 85/262 (32%), Positives = 98/262 (37%), Gaps = 85/262 (32%)

Frame = +3

Query: 537 SKLSNVATSVSNKSVRQDG--FXXXXXXXXXXXXXXXXXXXXC-----R 656

SKL+NVATSVSNKS + F C

Sbjct: 7 SKLTNVATSVSNKSQAKVSGMFARMGFAATDEEAVGFACDDLDLDFEHRQGLQMDILKSE 66

Query: 657 *EPCGDEGAEPVE----RQR-----SSSAALRLQGHSGATTSPKSR-----G 776

EPCGDEGAEPVE QR S A+ G G PK

Sbjct: 67 GEPCGDEGAEPVEGDIHYQRGGAPLPPSGSKDQAVGAGGEFGGHDKPKITAWAGWNVT 126

Query: 777 SAIQGMFVLGLPYAGVVSHHLRRRCVLPRAC----TRRMKTA-----RW 896

+AIQGMFVLGLPYA + +L ++ A T ++ A +

Sbjct: 127 NAIQGMFVLGLPYAILHGGYLGLFLIIFAAVVCCYTGKILIAclyEENEDGEVVRVRSY 186

Query: 897 WAIANACCAPRFPTRSADHRAGDDVHPASCTTASRGC----- 1007

AIANACCAPRFPT G V+ A C

Sbjct: 187 VAIANACCAPRFPT-----LGGRVVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQK 241

Query: 1008 --PCRSTAVLLPCAFLKNLSAV 1067

+TAVLLPCAFLKNL AV

Sbjct: 242 SWSIIATAVLLPCAFLKNLKA 263

Score = 72.0 bits (175), Expect = 4e-11

Identities = 120/441 (27%), Positives = 135/441 (30%), Gaps = 152/441 (34%)

Frame = +2

Query: 620 DDLDLFEHRQGLQXXXXXXXXXXXXXXXXXXXX-----XXCRPP-----APRT 739

DDLDLFEHRQGLQ PP A

Sbjct: 48 DDLDLFEHRQGLQMDILKSEGEPCGDEGAEPVEGDIHYQRGGAPLPPSGSKDQAVGAGGE 107

Query: 740 FGGHDKPKITAWERH-----PGHVRAgPTLRRGCFXXXXXXXX----- 853

FGGHDKPKITAW E P + G L G F

Sbjct: 108 FGGHDKPKITAWAGWNVTNAIQGMFVLGLPYAILHGGYL--GLFLIIFAAVVCCYTGKI 165

Query: 854 XXXXXYEENEDGEVV-----GHSQRLLRPALPN----A*XXXXXXXXXASC----- 979

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                YEENEDGEVV      +      P      P      +C
Sbjct: 166  LIACLYEENEDGEVVRVRSYVAIANACCAPRFPPTLGGRVVNVAQIIELVMTICILYVVVS 225

Query: 980  --LMYNSFPGLPVSQHG---RAAALRLP*EPLCCALWPTSSSIS----- 1096
                LMYNSFPGLPVSQ      A A+ LP      CA      ++S
Sbjct: 226  GNLMYNSFPGLPVSQKWSIIATAVLLP-----CAFLKNLKAWSKFSLLCTLAHFVINIL 280

Query: 1097  -----CPPRDWAWKVKFY-----HLHWHHRVQLHVSXXXXX-----XX 1198
                RDWAWKVKFY      + + + Q+ +
Sbjct: 281  VIAYCLSRARDWAWKVKFYIDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSEFHCMM 340

Query: 1199  XXXXXXXXVLKGLFALVAYXXXXXXXXX-----XXXXXXXXXXXXXXXXXXXXSLP--- 1339
                VLKGLFALVAY      LP
Sbjct: 341  NWTTHAACVLKGLFALVAYLTWADETKEVITDNLPGSIRAVVNLFLVAKALLSYPLPFFA 400

Query: 1340  -----SLFQEGSRAFFPAPEVLGADAALRARPFMCRTSRCS----- 1447
                SLFQEGSRAFFPA      G D L++      T RC+
Sbjct: 401  AVEVLEKSLFQEGSRAFFPA--CYGGDGRCLKSWGL---TLRCALVVFTLLMAIYVPHFAL 455

Query: 1448  -----WASPLCFLLP SLF 1486
                + LCFLLP SLF
Sbjct: 456  LMGLTGSLTGAGLCFLLP SLF 476

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Score = 70.1 bits (170), Expect(2) = 4e-23

Identities = 92/314 (29%), Positives = 101/314 (32%), Gaps = 101/314 (32%)

Frame = +1

```

Query: 580  FARMGFQAATDEEXXXXXXXXXXXXXDE-----SPAGTRALKRPSRGS----- 705
                FARMGFQAATDEE      +      P G      + P G
Sbjct: 28  FARMGFQAATDEEAVGFAHCDDLD FEHRQGLQMDILKSEGEPCGDEGAEPVEGDIHYQR 87

Query: 706  -GAPLPPSGSKDIRGPRQAQNHGVGAPSRAC--SCWAYPTP----- 819
                GAPLPPSGSKD      + G P      + W
Sbjct: 88  GGAPLPPSGSKDQAVGAGGEFGGHDKPKITAWGWNVTNAIQGMFVLGLPYAILHGGYL 147

Query: 820  GLFLIIIFAAXXXXXXXXXXXXXXXXXXXXXXXXXXQ-----R 939
                GLFLIIIFA      S
Sbjct: 148  GLFLIIIFAAVCCYTGKILIAclyEENEDGEVVRVRSYVAIANACCAPRFPPTLGGRVVN 207

Query: 940  VAQIIELVMTICILPHV-----QQLPGA-----ARVAARPCCLA---PSLRTS 1059
                VAQIIELVMTICIL V      PG      A      PC L      + S
Sbjct: 208  VAQIIELVMTICILYVVVSGNLMYNSFPGLPVSQKWSIIATAVLLPCAFLKNLKAWSKFS 267

Query: 1060  LLCTLAHFVINIL-----SSPRLGLGEGQVLPSPASSCSATRL 1176
                LLCTLAHFVINIL      + + G ++ S S L
Sbjct: 268  LLCTLAHFVINILVIAYCLSRARDWAWKVKFYIDVKKFPISIGIIVFS-YTSQIFLPSL 326

Query: 1177  RGNMQQPSEFHCMM 1218
                GNMQQPSEFHCMM
Sbjct: 327  EGNMQQPSEFHCMM 340

```

Score = 62.4 bits (150), Expect(2) = 4e-23

Identities = 52/136 (38%), Positives = 60/136 (44%), Gaps = 41/136 (30%)

Frame = +3

```

Query: 1254  TSEVITDNLPGSIRAGQGA VVLSAILC-----RRSSRKAAAPFS 1373

```


T EVITDNLPGSIRA +++ A+L R+ A
 Sbjct: 366 TKEVITDNLPGSIRAVVNLFVAKALLSYPLPFFAAVEVLEKSLFQEGSRAFFPACYGGD 425

Query: 1374 RPLKSWGLTLRCALVHLCAALRAAHGPH-----PSVSCC---PASF-----T 1490
 LKSWGLTLRCALV + L A + PH C P+ F
 Sbjct: 426 GRLKSWGLTLRCALV-VFTLLMAIYVPHFALLMGLTGSLTGAGLCFLLPSLFHLRLLWRK 484

Query: 1491 CAWHQVFFDVAIFVIG 1538
 WHQVFFDVAIFVIG
 Sbjct: 485 LLWHQVFFDVAIFVIG 500

Score = 35.8 bits (81), Expect = 3.0
 Identities = 27/74 (36%), Positives = 28/74 (37%), Gaps = 20/74 (27%)
 Frame = +1

Query: 1417 SIYVPHFALLMGLTPLFLAA-----QPLXXXXXXXXXXXXXXXXXX 1536
 +IYVPHFALLMGLT A
 Sbjct: 447 AIYVPHFALLMGLTGSLTGAGLCFLLPSLFHLRLLWRKLLWHQVFFDVAIFVIGGICSVS 506

Query: 1537 XFVHSLEGLIEAYR 1578
 FVHSLEGLIEAYR
 Sbjct: 507 GFVHSLEGLIEAYR 520

☐ >gi|26665359|dbj|BAC44888.1| vesicular GABA transporter a form [Mus musculus]
 Length = 521

Score = 72.8 bits (177), Expect = 2e-11
 Identities = 85/262 (32%), Positives = 98/262 (37%), Gaps = 85/262 (32%)
 Frame = +3

Query: 537 SKLSNVATSVSNKSVRQDG--FXXXXXXXXXXXXXXXXXXC-----R 656
 SKL+NVATSVSNKS + F C
 Sbjct: 7 SKLTNVATSVSNKSQAKVSGMFARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKSE 66

Query: 657 *EPCGDEGAEPVE----RQR-----SSSAALRLQGHSGATTSPKSRR-----G 776
 EPCGDEGAEPVE QR S A+ G G PK
 Sbjct: 67 GEPCGDEGAEPVEGDIHYQRGGAPLPPSGSKDQAVGAGGEFGGHDKPKITAWAGWNVT 126

Query: 777 SAIQGMFVLGLPYAGVVSHHLRRRCVLPRAC----TRRMKTA-----RW 896
 +AIQGMFVLGLPYA + +L ++ A T ++ A +
 Sbjct: 127 NAIQGMFVLGLPYAILHGGYLGLFLIIFAAVVCCYTGKILIACLYEENEDGEVVRVRSY 186

Query: 897 WAIANACCAPRFPTRSDHRAGDDVHPASCTTASRG-----1007
 AIANACCAPRFPT G V+ A C
 Sbjct: 187 VAIANACCAPRFPT-----LGGRVVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQK 241

Query: 1008 --PCRSTAVLLPCAFLKNLSAV 1067
 +TAVLLPCAFLKNL AV
 Sbjct: 242 SWSIIATAVLLPCAFLKNLKAV 263

Score = 72.0 bits (175), Expect = 4e-11
 Identities = 120/441 (27%), Positives = 135/441 (30%), Gaps = 152/441 (34%)
 Frame = +2

Query: 620 DDLD FEHRQGLQ MXXXXXXXXXXXXXXXXXXXXX-----XXCRPP-----APRT 739
 DDLD FEHRQGLQ M PP A
 Sbjct: 48 DDLD FEHRQGLQMDILKSEGEPCGDEGAEPVEGDIHYQRGGAPLPPSGSKDQAVGAGGE 107

Query: 740 FGGHDKPKITAWERH-----PGHVRAGPTLRRGCFXXXXXXXXXX----- 853
 FGGHDKPKITAW E P + G L G F
 Sbjct: 108 FGGHDKPKITAW EAGWNVTNAIQGMFVLGLPYAILHGGYL--GLFLIIFA AVVCCYTGKI 165

Query: 854 XXXXXYEENEDGEVV-----GHSQRLLRPALPN----A*XXXXXXXXXASC----- 979
 YEENEDGEVV + P P +C
 Sbjct: 166 LIACLYEENEDGEVVRV RDSYVAIANACCAPRFPTLGGRVVNVAQIIELVMT CILYVVVS 225

Query: 980 --LMYNSFPGLPVSQHG---RAAALRLP*EPLCCALWPTSSSIS----- 1096
 LMYNSFPGLPVSQ A A+ LP CA ++S
 Sbjct: 226 GNLMYNSFPGLPVSQKSWSI IATAVLLP-----CAFLKNLKA VSKFSL LCTLAHFVINIL 280

Query: 1097 -----CPPRDWAW EKVKFY-----HLHWHHRVQLHVS GXXXXX-----XX 1198
 RDWAW EKVKFY + + + Q+ +
 Sbjct: 281 VIAYCLSRARDWAW EKVKFYIDVKKFPISIGIIVFSYTSQIFLPSLEGNMQPSEFHCMM 340

Query: 1199 XXXXXXXXVLKGLFALVAYXXXXXXXXX-----XXXXXXXXXXXXXXXXXXXXXSLP--- 1339
 VLKGLFALVAY LP
 Sbjct: 341 NWT HIAACVLKGLFALVAYLTWADETKEVITDNLP GSIRAVVNLFVAKALLSYPLPFFA 400

Query: 1340 -----SLFQEGSRAFFPAPEVLGADAALRARPFMCRTSRCS----- 1447
 SLFQEGSRAFFPA G D L++ T RC+
 Sbjct: 401 AVEVLEKSLFQEGSRAFFPA--CYGGDGRLKSWGL---TLRCALVVFTLLMAIYVPHFAL 455

Query: 1448 -----WASPLCFLLP SLF 1486
 + LCFLLP SLF
 Sbjct: 456 LMGLTGSLTGAGLCFLLP SLF 476

Score = 70.1 bits (170), Expect(2) = 4e-23

Identities = 92/314 (29%), Positives = 101/314 (32%), Gaps = 101/314 (32%)

Frame = +1

Query: 580 FARMGFQAATDEEXXXXXXXXXXXXXXXXXDE-----SPAGTRALKRPSRGS----- 705
 FARMGFQAATDEE + P G + P G
 Sbjct: 28 FARMGFQAATDEEAVGFAHCDDLD FEHRQGLQMDILKSEGEPCGDEGAEPVEGDIHYQR 87

Query: 706 -GAPLPPSGSKDIRGPRQAQNHGVGAPSRAC--SCWAYPTP----- 819
 GAPLPPSGSKD + G P + W
 Sbjct: 88 GGAPLPPSGSKDQAVGAGGEFGGHDKPKITAW EAGWNVTNAIQGMFVLGLPYAILHGGYL 147

Query: 820 GLFLIIFAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSQ-----R 939
 GLFLIIFA A S
 Sbjct: 148 GLFLIIFA AVVCCYTGKIL IACLYEENEDGEVVRV RDSYVAIANACCAPRFPTLGGRVVN 207

Query: 940 VAQIIELVMT CILPHV-----QQLPGA-----ARVAARPCCCLA---PSLRTS 1059
 VAQIIELVMT CIL V PG A PC L + S
 Sbjct: 208 VAQIIELVMT CILYVVVSGNLMYNSFPGLPVSQKSWSI IATAVLLPCAFLKNLKA VSKF 267

Query: 1060 LLCTLAHFVINIL-----SSPRLGLGEGQVLPSP LASSCSATRL 1176
 LLCTLAHFVINIL + + G ++ S S L
 Sbjct: 268 LLCTLAHFVINILVIAYCLSRARDWAW EKVKFYIDVKKFPISIGIIVFS-YTSQIFLPSL 326

Query: 1177 RGNMQQPSEFHCMM 1218
 GNMQQPSEFHCMM

Sbjct: 327 EGNMQQPSEFHCMM 340

Score = 62.4 bits (150), Expect(2) = 4e-23
Identities = 52/136 (38%), Positives = 60/136 (44%), Gaps = 41/136 (30%)
Frame = +3

Query: 1254 TSEVITDNLPGSIRAGQGAVVLSSAILC-----RRSSRKAAAPFS 1373
T EVITDNLPGSIRA +++ A+L R+ A
Sbjct: 366 TKEVITDNLPGSIRAVVNLFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAFFPACYGGD 425

Query: 1374 RPLKSWGLTLRCALVHLCAALRAAHGPH-----PSVSCC---PASF-----T 1490
LKSWGLTLRCALV + L A + PH C P+ F
Sbjct: 426 GRLKSWGLTLRCALV-VFTLLMAIYVPHFALLMGLTGSALTGAGLCFLLPSLFHLRLLRK 484

Query: 1491 CAWHQVFFDVAIFVIG 1538
WHQVFFDVAIFVIG
Sbjct: 485 LLWHQVFFDVAIFVIG 500

☐ >gi|13929106|ref|NP_113970.1| ☒ vesicular inhibitory amino acid transporter [Rat
gi|34860244|ref|XP_346679.1| ☒ hypothetical protein XP_346678 [Rattus norvegicus]
gi|29428082|sp|O35458|VIAA_RAT ☒ Vesicular inhibitory amino acid transporter (GAB
transporter) (Vesicular GABA transporter) (rGVAT)
gi|2587061|gb|AAB82950.1| ☒ vesicular GABA transporter [Rattus norvegicus]
Length = 525

Score = 72.0 bits (175), Expect = 4e-11
Identities = 120/441 (27%), Positives = 135/441 (30%), Gaps = 152/441 (34%)
Frame = +2

Query: 620 DDLD FEHRQGLQ MXXXXXXXXX-----XXXXXXXXXXXXCRPP-----APRT 739
DDLD FEHRQGLQ M PP A
Sbjct: 48 DDLD FEHRQGLQMDILKSEGEPCGDEGAEPPEVDIHYQRGGAPLPSPGSKDQAVGAGGE 107

Query: 740 FGGHDKPKITAWERH-----PGHVRAGPTLRRGCFXXXXXXXXX----- 853
FGGHDKPKITAW E P + G L G F
Sbjct: 108 FGGHDKPKITAW EAGWNVNNAIQGMFVLGLPYAILHGGYL--GLFLIIFAAVVCCYTGKI 165

Query: 854 XXXXXYEENEDGEVV-----GHSQRLRLPALPN----A*XXXXXXXXXASC----- 979
YEENEDGEVV + P P +C
Sbjct: 166 LIACLYEENEDGEVVRVRSYVAIANACCAPREFPTLGGRVVNVAQIIELVMTCILYVVVS 225

Query: 980 --LMYNSFPGLPVSQHG---RAAALRLP*EPLCCALWPTSSSIS----- 1096
LMYNSFPGLPVSQ A A+ LP CA ++S
Sbjct: 226 GNLMYNSFPGLPVSQKSWSIATAVLLP-----CAFLKNLKA VSKFSL LCTLAHFVINIL 280

Query: 1097 -----CPPRDWAW EKVKFY-----HLHWHHRVQLHVS GXXXXX-----XX 1198
RDWAW EKVKFY + + + Q+ +
Sbjct: 281 VIAYCLSRARDWAW EKVKFYIDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSEFHCMM 340

Query: 1199 XXXXXXXXVLKGLFALVAYXXXXXXXXX-----XXXXXXXXXXXXXXXXXXXXSLP--- 1339
VLKGLFALVAY LP
Sbjct: 341 NWTTHIAACVLKGLFALVAYLTWADETKEVITDNLPGSIRAVVNIFLVAKALLSYPLPFFA 400

Query: 1340 -----SLFQEGSRAFFPAPEVLGADAALRARPFMCRTSRCS----- 1447
SLFQEGSRAFFPA G D L++ T RC+

Sbjct: 401 AVEVLEKSLFQEGSRAFFPA--CYGGDGRLLKSWGL---TLRCALVVFTLLMAIYVPHFAL 455

Query: 1448 -----WASPLCFLLP SLF 1486
+ LCFLLP SLF

Sbjct: 456 LMGLTGSLTGAGLCFLLP SLF 476

Score = 70.9 bits (172), Expect = 8e-11

Identities = 84/262 (32%), Positives = 97/262 (37%), Gaps = 85/262 (32%)

Frame = +3

Query: 537 SKLSNVATSVSNKSVRQDG--FXXXXXXXXXXXXXXXXXXXXC-----R 656
SKL+NVATSVSNKS + F C

Sbjct: 7 SKLTNVATSVSNKSQAKVSGMFARMGFQAATDEEAVGFACDDLD FEHRQGLQMDILKSE 66

Query: 657 *EPCGDEGAEPVE----RQR-----SSAALRLQGHSGATTSPKSRR-----G 776
EPCGDEGAEPVE QR S A+ G G PK

Sbjct: 67 GEPCGDEGAEPPEVDIHYQRGGAPLPPSGSKDQAVGAGGEFGGHDKPKITAEAGWNVT 126

Query: 777 SAIQGMFVLGLPYAGVVSHHLRRRCVLPRAC---TRRMKTA-----RW 896
+AIQGMFVLGLPYA + +L ++ A T ++ A +

Sbjct: 127 NAIQGMFVLGLPYAILHGGYLGLFLIIFAAVCCYTGKILIACLYEENEDGEVVRVRSY 186

Query: 897 WAIANACCAPRFPTRSADHRAGDDVHPASCTTASRGC-----1007
AIANACCAPRFPT G V+ A C

Sbjct: 187 VAIANACCAPRFPT-----LGGRVVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQK 241

Query: 1008 --PCRSTAVLLPCAFLKNLSAV 1067
+TAVLLPCAFLKNL AV

Sbjct: 242 SWSIIATAVLLPCAFLKNLKAV 263

Score = 69.7 bits (169), Expect(2) = 6e-23

Identities = 92/314 (29%), Positives = 101/314 (32%), Gaps = 101/314 (32%)

Frame = +1

Query: 580 FARMGFQAATDEEXXXXXXXXXXXXXDE-----SPAGTRALKRPSRGS-----705
FARMGFQAATDEE + P G + P G

Sbjct: 28 FARMGFQAATDEEAVGFACDDLD FEHRQGLQMDILKSEGEPCGDEGAEPPEVDIHYQR 87

Query: 706 -GAPLPPSGSKDIRGPRQAQNHGVGAPSRAC--SCWAYPTP-----819
GAPLPPSGSKD + G P + W

Sbjct: 88 GGAPLPPSGSKDQAVGAGGEFGGHDKPKITAEAGWNVTNAIQGMFVLGLPYAILHGGYL 147

Query: 820 GLFLIIFAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSQ-----R 939
GLFLIIFAA S

Sbjct: 148 GLFLIIFAAVCCYTGKILIACLYEENEDGEVVRVRSYVAIANACCAPRFPTLGGRVVN 207

Query: 940 VAQIIELVMTCILPHV-----QQLPGA-----ARVAARPCCLA---PSLRTS 1059
VAQIIELVMTCIL V PG A PC L + S

Sbjct: 208 VAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQKSWSIATAVLLPCAFLKNLKAVSKFS 267

Query: 1060 LLCTLAHFVINIL-----SSPRLGLGEGQVLPSPPLASSCSATRL 1176
LLCTLAHFVINIL + + G ++ S S L

Sbjct: 268 LLCTLAHFVINILVIAYCLSRARDWAWKVKFYIDVKKFPISIGIIVFS-YTSQIFLPSL 326

Query: 1177 RGNMQQPSEFHCM 1218
GNMQQPSEFHCM

Sbjct: 327 EGNMQQPSEFHCMM 340

Score = 62.4 bits (150), Expect(2) = 6e-23
Identities = 52/136 (38%), Positives = 60/136 (44%), Gaps = 41/136 (30%)
Frame = +3

Query: 1254 TSEVITDNLPGSIRAGQGAVVLSSAILC-----RRSSRKAAAPFS 1373

T EVITDNLPGSIRA +++ A+L R+ A

Sbjct: 366 TKEVITDNLPGSIRAVVNI FLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAFFPACYGGD 425

Query: 1374 RPLKSWGLTLRCALVHLCAALRAAHGPH-----PSVSCC---PASF-----T 1490

LKSWGLTLRCALV + L A + PH C P+ F

Sbjct: 426 GRLKSWGLTLRCALV-VFTLLMAIYVPHFALLMGLTGSLTGAGLCFLLPSLFHLRLLRK 484

Query: 1491 CAWHQVFFDVAIFVIG 1538

WHQVFFDVAIFVIG

Sbjct: 485 LLWHQVFFDVAIFVIG 500

Score = 35.8 bits (81), Expect = 3.0
Identities = 27/74 (36%), Positives = 28/74 (37%), Gaps = 20/74 (27%)
Frame = +1

Query: 1417 SIYVPHFALLMGLTPLFLAA-----QPLXXXXXXXXXXXXXXXXXX 1536

+IYVPHFALLMGLT A

Sbjct: 447 AIYVPHFALLMGLTGSLTGAGLCFLLPSLFHLRLLRKLLWHQVFFDVAIFVIGGICSVS 506

Query: 1537 XFVHSLEGLIEAYR 1578

FVHSLEGLIEAYR

Sbjct: 507 GFVHSLEGLIEAYR 520

☐ >gi|6678569|ref|NP_033534.1| ☒ vesicular inhibitory amino acid transporter [Mus
gi|2826776|emb|CAA04864.1| ☒ vesicular inhibitory amino acid transporter [Mus mus
Length = 521

Score = 72.8 bits (177), Expect = 2e-11
Identities = 85/262 (32%), Positives = 98/262 (37%), Gaps = 85/262 (32%)
Frame = +3

Query: 537 SKLSNVATSVSNKSVRQDG--FXXXXXXXXXXXXXXXXXXC-----R 656

SKL+NVATSVSNKS + F C

Sbjct: 7 SKLTVNATSVSNKSQAKVSGMFARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKSE 66

Query: 657 *EPCGDEGAEPVE----RQR-----SSAALRLQGHSGATTSPKSRR-----G 776

EPCGDEGAEPVE QR S A+ G G PK

Sbjct: 67 GEPCGDEGAEPVEGDIHYQRGGAPLPPSGSKDQAVGAGGEFGGHDKPKITAWAGWNV 126

Query: 777 SAIQGMFVLGLPYAGVVSHHLRRRCVLPRAC----TRRMKTA-----RW 896

+AIQGMFVLGLPYA + +L ++ A T ++ A +

Sbjct: 127 NAIQGMFVLGLPYAILHGGYLGFLIIFAAVCCYTGKILIACLYEENEDGEVVRVRSY 186

Query: 897 WAIANACCAPRFPTRSADHRAGDDVHPASCTTASRG----- 1007

AIANACCAPRFPT G V+ A C

Sbjct: 187 VAIANACCAPRFPT-----LGGRVVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQK 241

Query: 1008 --PCRSTAVLLPCAFLKNLSAV 1067
+TAVLLPCAFLKNL AV
Sbjct: 242 SWSIIATAVLLPCAFLKNLKAV 263

Score = 72.4 bits (176), Expect = 3e-11
Identities = 120/441 (27%), Positives = 135/441 (30%), Gaps = 152/441 (34%)
Frame = +2

Query: 620 DDLDFEHRQGLQMXXXXXXXXXXXXXXXXXX-----XXCRPP-----APRT 739
DDLDFEHRQGLQM PP A
Sbjct: 48 DDLDFEHRQGLQMDILKSEGEPCGDEGAEAPVEGDIHYQRGGAPLPPSGSKDQAVGAGGE 107

Query: 740 FGGHDKPKITAWERH-----PGHVRAGPTLRRGCFXXXXXXXXX----- 853
FGGHDKPKITAW E P + G L G F
Sbjct: 108 FGGHDKPKITAW EAGWNVNTNAIQGMFVLGLPYAILHGGYL--GLFLIIFA AVVCCYTGKI 165

Query: 854 XXXXXYEENEDGEVV-----GHSQRLRLPALPN----A*XXXXXXXXXASC----- 979
YEENEDGEVV + P P +C
Sbjct: 166 LIACLYEENEDGEVVRVRSYVAIANACCAPRFPTLGGRVVNVAQIIELVMTCILYVVVS 225

Query: 980 --LMYNSFPGLPVSQHG---RAAALRLP*EPLCCALWPTSSSIS----- 1096
LMYNSFPGLPVSQ A A+ LP CA ++S
Sbjct: 226 GNLMYNSFPGLPVSQKSWSIATAVLLP-----CAFLKNLKAVSKFSLLECTLAHFVINIL 280

Query: 1097 -----CPPRDWAEKVKFY-----HLHWHHRVQLHVSGXXXX-----XX 1198
RDWAEKVKFY + + + Q+ +
Sbjct: 281 VIAYCLSRARDWAEKVKFYIDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSEFHCMM 340

Query: 1199 XXXXXXXXVLKGLFALVAYXXXXXXXX-----XXXXXXXXXXXXXXXXXXXXSLP--- 1339
VLKGLFALVAY LP
Sbjct: 341 NWTHIAACVLKGLFALVAYLTWADETKEVITDNLPGSIRAVVNLFLVAKALLSYPLPFFA 400

Query: 1340 -----SLFQEGSRAFFPAPEVLGADAALRARPFMCRTSRCS----- 1447
SLFQEGSRAFFPA G D L++ T RC+
Sbjct: 401 AVEVLEKSLFQEGSRAFFPA--CYGGDGRLKSWEL---TLRCALVVFTLLMAIYVPHFAL 455

Query: 1448 -----WASPLCFLLP SLF 1486
+ LCFLLP SLF
Sbjct: 456 LMGLTGSLTGAGLCFLLP SLF 476

Score = 70.1 bits (170), Expect(2) = 4e-22
Identities = 92/314 (29%), Positives = 101/314 (32%), Gaps = 101/314 (32%)
Frame = +1

Query: 580 FARMGFQAATDEEXXXXXXXXXXXXXDE-----SPAGTRALKRPSRGS----- 705
FARMGFQAATDEE + P G + P G
Sbjct: 28 FARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKSEGEPCGDEGAEAPVEGDIHYQR 87

Query: 706 -GAPLPPSGSKDIRGPRQAQNHGVGAPSRAC--SCWAYPTP----- 819
GAPLPPSGSKD + G P + W
Sbjct: 88 GGAPLPPSGSKDQAVGAGGEFGGHDKPKITAW EAGWNVNTNAIQGMFVLGLPYAILHGGYL 147

Query: 820 GLFLIIFAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSQ-----R 939
GLFLIIFA S
Sbjct: 148 GLFLIIFA AVVCCYTGKILIACLYEENEDGEVVRVRSYVAIANACCAPRFPTLGGRVVN 207

Query: 940 VAQIIELVMTCILPHV-----QQLPGA-----ARVAARPCCCLA---PSLRTS 1059
 VAQIIELVMTCIL V PG A PC L + S
 Sbjct: 208 VAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQKWSIIATAVLLPCAFLKNLKAIVSKFS 267

Query: 1060 LLCTLAHFVINIL-----SSPRLGLGEGQVLPSPASSCSATRL 1176
 LLCTLAHFVINIL + + G ++ S S L
 Sbjct: 268 LLCTLAHFVINILVIAYCLSRARDWAWEKVKFYIDVKKFPISIGIIVFS-YTSQIFLPSL 326

Query: 1177 RGNMQQPSEFHCMM 1218
 GNMQQPSEFHCMM
 Sbjct: 327 EGNMQQPSEFHCMM 340

Score = 59.3 bits (142), Expect(2) = 4e-22
 Identities = 51/136 (37%), Positives = 59/136 (43%), Gaps = 41/136 (30%)
 Frame = +3

Query: 1254 TSEVITDNLPGSIRAGQGA VLLSSAILC-----RRSSRKAAAPFS 1373
 T EVITDNLPGSIRA +++ A+L R+ A
 Sbjct: 366 TKEVITDNLPGSIRAVVNLFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAFFPACYGGD 425

Query: 1374 RPLKSWGLTLRCALVHLCAALRAAHGPH-----PSVSCC---PASF-----T 1490
 LKSW LTLRCALV + L A + PH C P+ F
 Sbjct: 426 GRLKSWELTLRCALV-VFTLLMAIYVPHFALLMGLTGSLTGAGLCFLLPSLFHLRLLRK 484

Query: 1491 CAWHQVFFDVAIFVIG 1538
 WHQVFFDVAIFVIG
 Sbjct: 485 LLWHQVFFDVAIFVIG 500

☐ >gi|34785016|gb|AAH36458.2| ☒ VIAAT protein [Homo sapiens]
 Length = 475

Score = 69.3 bits (168), Expect = 2e-10
 Identities = 71/201 (35%), Positives = 81/201 (40%), Gaps = 65/201 (32%)
 Frame = +3

Query: 660 EPCGDEGAEPVE----RQRSSSAALRLQGH-----GATTSPKSRR-----GS 779
 EPCGDEGAEPVE QR S A L G G PK +
 Sbjct: 18 EPCGDEGAEPVEGDIHYQRGSGAPLPPSGSKDQVGGGGEFGGHDKPKITAWAGWNVTN 77

Query: 780 AIQGMFVLGLPYAGVVS HHLRRRCVLPAC----TRRMKTA-----RWW 899
 AIQGMFVLGLPYA + +L ++ A T ++ A +
 Sbjct: 78 AIQGMFVLGLPYAILHGGYLGLFLIIFA VVCCYT GKIL IACLYEENEDGEVVRVRDSYV 137

Query: 900 AIANACCAPRFPTRSADHRAGDDVHPASCTTASRGC----- 1007
 AIANACCAPRFPT G V+ A C
 Sbjct: 138 AIANACCAPRFPT-----LGGRVVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQKS 192

Query: 1008 -PCRSTAVLLPCAFLKNLSAV 1067
 +TAVLLPCAFLKNL AV
 Sbjct: 193 WSIIATAVLLPCAFLKNLRVAV 213

Score = 64.3 bits (155), Expect(2) = 2e-21
 Identities = 81/256 (31%), Positives = 90/256 (35%), Gaps = 82/256 (32%)

